

SEQUENCE LISTING

<110> CROCE, Carlo M.
ISHII, Hideshi

<120> COMPOSITIONS, KITS, AND METHODS RELATING TO THE HUMAN
FEZ1 GENE, A NOVEL TUMOR SUPPRESSOR GENE

<130> 9855-30U1 (209855.0081)

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<150> US 60/121,537

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<170> PatentIn Ver. 2.1

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<210> 11

<211> 1614

<212> DNA

<213> Homo sapiens

<400> 11

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tccccggaga gtgccagcca ccagctgcac cccgcccctc cagacaagcc caaggagcag 480
gagctgaagc ctggcctgtg ctctggggcg ctgtcagact ccggccggaa ctccatgtcc 540
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<210> 12

<211> 1512

<212> DNA

<213> Homo sapiens

<400> 12

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gattacacgg	cactgtccag	cggggattta	gggggccagg	ctgggggtgga	ctttgaccgc	300
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<210> 13
<211> 1692
<212> DNA
<213> Homo sapiens

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gacagcaaca tgatgagcct gaaggctctg tcttctccg acggaggtag caagctgggc 720
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<211> 1722
<212> DNA
<213> Homo sapiens

<400> 14

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<211> 76

<213> Homo sapiens

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His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
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Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
35 40 45

Asp Ser Gly His Gly Lys Ala Met Thr Arg Cys Pro Arg Ala Ser Ser
50 55 60

[illegible]

16

205

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln
180 185 190

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Ser	Ala	His	Asn	Ile	Thr	Gln	Gly	Ile	Val	Leu	Gln	Asp	Ser	Asn	Met
210						215						220			
Met	Ser	Leu	Lys	Ala	Leu	Ser	Phe	Ser	Asp	Gly	Gly	Ser	Lys	Leu	Gly
225						230						240			
His	Ser	Asn	Lys	Ala	Asp	Lys	Gly	Pro	Ser	Cys	Val	Arg	Ser	Pro	Ile
			245						250			255			
Ser	Thr	Asp	Glu	Cys	Ser	Ile	Gln	Glu	Leu	Glu	Gln	Lys	Leu	Leu	Glu
			260						265			270			
Arg	Glu	Gly	Ala	Leu	Gln	Lys	Leu	Gln	Arg	Ser	Phe	Glu	Glu	Lys	Glu
			275						280			285			
Leu	Ala	Ser	Ser	Leu	Ala	Tyr	Glu	Glu	Arg	Pro	Arg	Arg	Cys	Arg	Asp
290						295						300			
Glu	Leu	Glu	Gly	Pro	Glu	Pro	Lys	Gly	Gly	Asn	Lys	Leu	Lys	Gln	Ala
305						310						315			
Ser	Gln	Lys	Ser	Gln	Arg	Ala	Gln	Gln	Val	Leu	His	Leu	Gln	Val	Leu
			325						330			335			
Gln	Leu	Gln	Gln	Glu	Lys	Arg	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu
			340						345			350			
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355						360						365			
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370						375						380			
Cys	Gln	Lys	Ser	Gly	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Gln	Leu	Lys	Glu
385						390						395			
Ser	Gln	Thr	Glu	Val	Asn	Ala	Lys	Ala	Ser	Glu	Ile	Leu	Gly	Leu	Lys
			405						410			415			
Ala	Gln	Leu	Lys	Asp	Thr	Arg	Gly	Lys	Leu	Glu	Gly	Leu	Glu	Leu	Arg
			420						425			430			
Thr	Gln	Asp	Leu	Glu	Gly	Ala	Leu	Arg	Thr	Lys	Gly	Leu	Glu	Leu	Glu
435						440						445			

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
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 Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
 145 150 155 160
 Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
 165 170 175
 Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln
 180 185 190
 Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly
 195 200 205
 Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met
 210 215 220
 Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly
 225 230 235 240
 His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile
 245 250 255
 Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu
 260 265 270
 Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu
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 Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp
 290 295 300
 Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala
 305 310 315 320
 Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu
 325 330 335
 Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu
 340 345 350
 Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg
 355 360 365
 Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val
 370 375 380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu
385 390 395 400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys
405 410 415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg
420 425 430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
435 440 445

Val Cys Glu Asn Glu Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg
450 455 460

Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser
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Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr
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Glu Asp Ile Ile Ala Thr Glu Ile
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<210> 19

<211> 563

<212> PRT

<213> Homo sapiens

<400> 19

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His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
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Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
50 55 60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val

95

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu

340	345	350
Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg		
355	360	365
Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val		
370	375	380
Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu		
385	390	395 400
Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys		
405	410	415
Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg		
420	425	430
Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu		
435	440	445
Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu		
450	455	460
Arg Glu Lys Val Asn Leu Leu Glu Arg Leu Arg Ala Glu Leu Arg Glu		
465	470	475 480
Glu Arg Gln Gly His Asp Gln Met Ser Ser Gly Phe Gln His Glu Arg		
485	490	495
Leu Val Trp Lys Glu Glu Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln		
500	505	510
Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu		
515	520	525
Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu		
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Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala		
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Thr Glu Ile		

<210> 20
 <211> 573
 <212> PRT

<213> Homo sapiens

<400> 20

Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
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His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
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Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
50 55 60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
85 90 95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
100 105 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
130 135 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
145 150 155 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
165 170 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln
180 185 190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly
195 200 205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met
210 215 220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly
225 230 235 240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile
 245 250 255
 Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu
 260 265 270
 Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu
 275 280 285
 Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp
 290 295 300
 Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala
 305 310 315 320
 Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu
 325 330 335
 Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu
 340 345 350
 Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg
 355 360 365
 Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val
 370 375 380
 Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu
 385 390 395 400
 Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys
 405 410 415
 Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg
 420 425 430
 Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
 435 440 445
 Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu
 450 455 460
 Arg Glu Lys Val Asn Leu Leu Glu Gln Glu Leu Gln Glu Leu Arg Ala
 465 470 475 480
 Gln Ala Ala Leu Ala Arg Asp Met Gly Pro Pro Thr Phe Pro Glu Asp
 485 490 495

Val Pro Ala Leu Gln Arg Glu Leu Glu Arg Leu Val Trp Lys Glu Glu
 500 505 510

Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val
 515 520 525

Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu
 530 535 540

Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly
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Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala Thr Glu Ile
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<210> 21

<211> 591

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: F37 Probe

<400> 21

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 tatgggggca tctcttcccc agagaggcac tcagtgagcc tcctgtgcoct ggccccagtc 180
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 gcttttgaca gcttcatttt atttttgacg tcactttttg gccatgtaaa ctatttgtgg 540
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<210> 22

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable
 region amplificatin primer G12

<400> 22

gctgccacag cctttccaag acc

23

<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G13

<400> 23
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23

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G14.2

<400> 24
acagcttcca cagcaagcac tgc

23

<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G15

<400> 25
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21

<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable

region amplification primer G16

<400> 26
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<210> 27
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer IntABR

<400> 27
gtttccaacc cacttaccct tgc 23

<210> 28
<211> 21
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer IntABF

<400> 28
gcaggggagg catgagtcac c 21

<210> 29
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G17

<400> 29
ggcttcagct cctgctcctt gg 22

<210> 30
<211> 23
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G20

<400> 30

acaacatcac ccagggcatc gtc

23

<210> 31

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G21

<400> 31

cctccagctc gtcctgcag c

21

<210> 32

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G32

<400> 32

actgcagctt cagcaggaga agc

23

<210> 33

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer IntBCR

<400> 33

ctgaccaccc aaacccatga gc

22

<210> 34
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer IntBCF

<400> 34
tcacctcttg gcactctgtc tcc

23

<210> 35
<211> 21
<212> DNA
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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer Mut6

<400> 35
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21

<210> 36
<211> 23
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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G1

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<210> 37
<211> 22
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region amplification primer G2

<400> 37
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<210> 38
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region amplification primer G75

<400> 38
cccaccttcc ccgaggacgt c 21

<210> 39
<211> 23
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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G82

<400> 39
agccccgagga catctggtca tgg 23

<210> 40
<211> 24
<212> DNA
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region amplification primer G5

<400> 40
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<210> 41
<211> 23
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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G6

<400> 41

agctgctgca gggccttctc cag

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<210> 42

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G7

<400> 42

cagtaccaga aacagctgca gcagagc

27

<210> 43

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G8

<400> 43

ccctgcctcc cagtgccagg tc

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<210> 44

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: First strand
of partially-double stranded adapter-linker

<400> 44

gatctcgacg aattcgtgag acct

24

<210> 45
<211> 20
<212> DNA
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<223> Description of Artificial Sequence: Second strand
of partially-double stranded adapter-linker

<400> 45
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<210> 46
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<212> DNA
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<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 46
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23

<210> 47
<211> 21
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 47
gagcggcaag gccatgacca g

21

<210> 48
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 48
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<210> 49
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<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 49
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<210> 50
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<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 50
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<210> 51
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<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

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<210> 52
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<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 52

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23

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 53

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<210> 54

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 54

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<210> 55

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 55

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<210> 56

<211> 24
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 <223> Description of Artificial Sequence: Donor site
 sequence of truncated FEZ1 truncation region

<400> 56
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<210> 57
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 <223> Description of Artificial Sequence: Acceptor site
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<400> 57
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<210> 58
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 <223> Description of Artificial Sequence: Primer for
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<400> 58
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<210> 59
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<400> 59

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<210> 60

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<223> Description of Artificial Sequence: Nucleotide
sequence of vector pQBI-AdCMV5-IRES-GFP

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